## CLAIMS

What is claimed is:

1. A method for detecting the presence of at least one selected strain of an organism in a sample, comprising the steps of:

providing a sample that may comprise nucleic acid from at least one selected strain of an organism and nucleic acid from at least one non-selected strain of the organism;

providing a plurality of primers substantially complementary to regions of both said nucleic acid from at least one selected strain of the organism and said nucleic acid from at least one non-selected strain of the organism;

exposing said sample to at least one probe that is sufficiently complementary to a portion of said nucleic acid from at least one non-selected strain to block full length amplification of said nucleic acid from at least one non-selected strain between said plurality of primers, said at least one probe comprising a nucleic acid analog;

amplifying said nucleic acid from at least one selected strain between said plurality of primers; and

detecting amplification product of nucleic acid from at least one selected strain.

2. The method of claim 1, wherein said at least one selected strain comprises a pathogenic strain.

3. The method of claim 2, wherein said sample is derived from a subject and said pathogenic strain indicates a risk of cancerous growth in said subject.

4. The method of claim 1, wherein said organism comprises human papilloma virus (HPV).

5. The method of claim 1, wherein said at least one probe comprises PNA.

6. The method of claim 5, wherein said at least one probe further comprises a nucleotide different from PNA.

7. The method of claim 1, wherein each of said at least one probe comprises at least 8 bases.

8. The method of claim 1, wherein the step of amplifying said nucleic acid of at least one selected strain between said plurality of primers comprises conducting a reaction selected from the group consisting of a polymerase chain reaction, a ligase chain reaction, a rolling circle replication, a branched chain amplification, a nucleic acid based sequence amplification (NASBA), a Cleavase Fragment Length Polymorphism, ICAN and RAM .

9. The method of claim 4, wherein said regions of both said nucleic acids are parts of a region selected from the group consisting of L1, L2, E1, E6, and E7 region.

10. The method of claim 4, wherein said at least one non-selected strain equals all the low-risk HPV strains known.

11. The method of claim 4, wherein said at least one non-selected strain is selected from the group consisting of HPV strains 6, 11, 42, 43, and 44.

12. The method of claim 4, wherein said at least one selected strain comprises a plurality of high-risk HPV strains.

13. The method of claim 4, wherein said plurality of primers comprise MY09 and MY11 (SEQ. ID. NOS. 10 and 11).

14. The method of claim 4, wherein said at least one probe is selected from the group of sequences consisting of SEQ. ID. NO. 6 and SEQ. ID. NO. 7.

15. The method of claim 1, wherein said sample is a cervical scraping.

16. The method of claim 1, wherein said step of detecting amplification product comprises in-gel electrophoresis of said product and staining said product with ethidium bromide.

17. A method for detecting the presence of a target nucleic acid of a human papilloma virus (HPV) in a sample cell, comprising the steps of:

suspending a sample cell in a solution;

isolating a target nucleic acid of a HPV from said sample cell;

contacting said target nucleic acid with at least one probe comprising peptide nucleic acid (PNA), said at least one probe being substantially complementary to portions of nucleic acids of multiple HPV types; and

detecting hybridization between said at least one probe and said target nucleic acid.

18. The method of claim 1, wherein said solution contains an alcohol in an amount sufficient to fix sample cells without coagulation, an anti-clumping agent, and a buffer agent that maintains the solution at a pH within a range of about 4 to about 7.

19. The method of claim 1, wherein said sample cells come from a subject and wherein the presence of said target nucleic acid sequence indicates a risk of tumor growth in said subject.

20. The method of claim 4, wherein said tumorous growth is associated with either cervical cancer or endocervical carcinoma.

21. The method of claim 3, wherein the presence of said target nucleic acid sequence is indicative of the presence of a particular type of HPV.

22. The method of claim 7, wherein said particular type of HPV is selected from the group consisting of types 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 68 and 70.

23. The method of claim 3, wherein absence of said target nucleic acid sequence is diagnostic of absence of infection by HPV.

24. The method of claim 3, wherein absence of said target nucleic acid sequence is diagnostic of absence of infection by HPV types selected from the group consisting of types 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 68 and 70.

25. The method of claim 1, wherein absence of said target nucleic acid sequence is diagnostic of absence of infection by high-risk types of HPV.

26. The method of claim 1, further comprising amplification of said target nucleic acid.

27. The method of claim 12, wherein said amplification step comprises conducting a polymerase chain reaction.

28. The method of claim 1, further comprising capturing said target nucleic acid onto a solid support through PNA-DNA interaction.

29. The method of claim 1, wherein each of said at least one probe comprises at least 8 bases.

30. The method of claim 1, wherein said at least one probe comprises a nucleotide different from PNA.

31. The method of claim 1, wherein said at least one probe is selected from the group consisting of SEQ. ID. NOS. 1-5.

32. The method of claim 1, wherein said at least one probe is labeled with a detectable marker.

33. The method of claim 17 wherein said at least one probe comprises a molecular beacon probe.

34. The method of claim 1, further comprising using an antibody to recognize said hybridization.

35. A method for detecting the presence of a target nucleic acid of a human papilloma virus (HPV) in a sample, comprising the steps of:

capturing candidate nucleic acids that include a target nucleic acid on a solid support;

contacting said candidate nucleic acids with at least one probe comprising peptide nucleic acid (PNA), said at least one probe being substantially complementary to portions of nucleic acids of multiple HPV types; and

detecting hybridization between said at least one probe and a target nucleic acid.

36. The method of claim 20, wherein capturing candidate nucleic acids comprises DNA-DNA interaction.

37. A method for in situ detection of the presence of a target nucleic acid of a human papilloma virus (HPV) in a sample, comprising the steps of:

transferring suspended sample cells uniformly onto a surface;

in situ hybridizing a target nucleic acid of a HPV contained in said cells with at least one probe comprising peptide nucleic acid (PNA), said at least one probe being substantially complementary to portions of nucleic acids of multiple HPV types; and

detecting hybridization between said at least one probe and a target nucleic acid.